==========
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2009; month=4; day=18; hr=17; min=11; sec=40; ms=976;]
==========

Validated By CRFValidator v 1.0.3

Application No: 10539954 Version No: 3.0

Input Set:

Output Set:

Started: 2009-04-02 15:10:34.399
Finished: 2009-04-02 15:10:39.189
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 790 ms
Total Warnings: 29
Total Errors: 1
No. of SeqIDs Defined: 88
Actual SeqID Count: 88

Error code		Error Description
W	402	Undefined organism found in <213> in SEQ ID (3)
W	402	Undefined organism found in <213> in SEQ ID (4)
W	402	Undefined organism found in <213> in SEQ ID (5)
W	402	Undefined organism found in <213> in SEQ ID (6)
W	402	Undefined organism found in <213> in SEQ ID (7)
W	402	Undefined organism found in <213> in SEQ ID (8)
W	402	Undefined organism found in <213> in SEQ ID (9)
W	402	Undefined organism found in <213> in SEQ ID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (21)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (21)
W	213	Artificial or Unknown found in <213> in SEQ ID (22)
W	213	Artificial or Unknown found in <213> in SEQ ID (27)
W	213	Artificial or Unknown found in <213> in SEQ ID (28)
W	213	Artificial or Unknown found in <213> in SEQ ID (29)
W	213	Artificial or Unknown found in <213> in SEQ ID (30)
W	213	Artificial or Unknown found in <213> in SEQ ID (31)
W	213	Artificial or Unknown found in <213> in SEQ ID (32)
W	213	Artificial or Unknown found in <213> in SEQ ID (33)
W	402	Undefined organism found in <213> in SEQ ID (49)

Input Set:

Output Set:

Started: 2009-04-02 15:10:34.399
Finished: 2009-04-02 15:10:39.189
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 790 ms
Total Warnings: 29
Total Errors: 1
No. of SeqIDs Defined: 88
Actual SeqID Count: 88

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (55)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 402	Undefined organism found in <213> in SEQ ID (61)
W 402	Undefined organism found in <213> in SEQ ID (77)
W 402	Undefined organism found in <213> in SEQ ID (79)
W 402	Undefined organism found in <213> in SEQ ID (80)
W 402	Undefined organism found in <213> in SEQ ID (82)
W 402	Undefined organism found in <213> in SEQ ID (85)
W 402	Undefined organism found in <213> in SEQ ID (88)

SEQUENCE LISTING

<110> Schmitz, Oliver
Puzio, Piotr
Blau, Astrid
Looser, Ralf
Wendel, Birgit
Kamlage, Beate
Plesch, Gunnar

<120> Method for Producing Amino Acids

<130> 13195-00006-US

<140> 10539954
<141> 2005-06-17

<150> PCT/EP2003/014649
<151> 2003-12-19

<150> DE 102 61 188.2
<151> 2002-12-20

<160> 88

<170> PatentIn version 3.3

<210> 1
<211> 1164
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(1164)
<223> Threonine aldolase

<400> 1

```
atg act gaa ttc gaa ttg cct cca aaa tat atc acc gct gct aac gac       48
Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp
1               5                   10                  15

ttg cgg tca gac aca ttc acc act cca act gca gag atg atg gag gcc       96
Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala
            20                  25                  30

gct tta gag gcc tct atc ggt gac gct gtc tac ggt gaa gat gtt gac      144
Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
        35                  40                  45

acc gtt agg ctc gaa cag acc gtt gcc cgc atg gct ggc aaa gaa gca      192
Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
    50                  55                  60

ggt ttg ttc tgt gtc tct ggg act ttg tcc aac cag att gcc atc aga      240
```

```
Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
65                  70                  75                  80

act cac ttg atg caa cct cca tac tct att cta tgt gat tac agg gct      288
Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala
                85                  90                  95

cac gtt tac act cac gaa gcc gct gga ctg gcg atc ttg tct caa gcg      336
His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala
            100                 105                 110

atg gtg gtt cct gtg gtt cct tcc aac ggt gac tac ttg acc ttg gaa      384
Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu
        115                 120                 125

gac atc aag tca cac tac gtc cca gac gac ggt gat att cac ggt gcc      432
Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala
    130                 135                 140

ccc acc aga ttg att tct ctg gaa aac act tta cac ggt att gtt tat      480
Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr
145                 150                 155                 160

cca ttg gaa gaa ctg gtc cgc atc aaa gct tgg tgt atg gaa aat ggt      528
Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly
                165                 170                 175

ctc aaa cta cat tgt gac ggt gcc aga atc tgg aat gcc gct gca caa      576
Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln
            180                 185                 190

tct ggc gtg cca tta aag caa tat ggg gaa atc ttc gac tcc atc tcc      624
Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser
        195                 200                 205

atc tgt cta tcc aag tct atg ggt gct cct att ggg tcc gtc ttg gtt      672
Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val
    210                 215                 220

ggg aac ctt aag ttt gtc aag aag gcc acc cat ttc aga aaa caa caa      720
Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln
225                 230                 235                 240

ggt ggt ggt att aga caa tct ggt atg atg gct aga atg gct ctt gta      768
Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val
                245                 250                 255

aac atc aac aac gat tgg aag tcc caa ttg ctg tac tcg cac tct ttg      816
Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu
            260                 265                 270

gct cat gaa tta gcc gaa tat tgt gag gca aag ggc atc ccg cta gag      864
Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu
        275                 280                 285

tct cca gca gac acc aac ttt gtc ttt att aac ctg aag gcc gct aga      912
Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg
```

```
    290                 295                 300

atg gac cca gat gtc ctt gtt aag aag ggt ttg aag tac aac gtt aag      960
Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys
305                 310                 315                 320

cta atg ggt ggt aga gtc tcg ttc cac tat caa gtc acc aga gat act     1008
Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr
                325                 330                 335

ttg gaa aaa gtc aaa ttg gcc atc tcc gag gcc ttc gac tat gct aaa     1056
Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys
            340                 345                 350

gaa cat cct ttc gac tgt aac gga cct acc cag att tac cgt agt gaa     1104
Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
        355                 360                 365

tcc acc gag gtc gac gtt gat ggc aac gct atc cgc gaa ata aaa acc     1152
Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
    370                 375                 380

tac aaa tac tga                                                    1164
Tyr Lys Tyr
385
```

<210> 2
<211> 387
<212> PRT
<213> Saccharomyces cerevisiae

<400> 2

```
Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp
1               5                   10                  15

Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala
            20                  25                  30

Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
        35                  40                  45

Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
    50                  55                  60

Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
65                  70                  75                  80

Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala
                85                  90                  95

His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala
            100                 105                 110

Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu
        115                 120                 125
```

```
Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala
    130                 135                 140

Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr
145                 150                 155                 160

Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly
                165                 170                 175

Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln
            180                 185                 190

Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser
        195                 200                 205

Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val
    210                 215                 220

Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln
225                 230                 235                 240

Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val
                245                 250                 255

Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu
            260                 265                 270

Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu
        275                 280                 285

Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg
    290                 295                 300

Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys
305                 310                 315                 320

Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr
                325                 330                 335

Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys
            340                 345                 350

Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
        355                 360                 365

Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
    370                 375                 380

Tyr Lys Tyr
385
```

<210> 3
<211> 376
<212> PRT
<213> Canola

<400> 3

```
Gly Cys Phe Ala Cys Tyr Leu Val Gly Gly Phe Ser Val Gln Glu Lys
1               5                  10                  15

Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro
            20                  25                  30

Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp
        35                  40                  45

Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala
    50                  55                  60


Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met
65                  70                  75                  80

Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu
                85                  90                  95

Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly
            100                 105                 110

Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp
        115                 120                 125

Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro
    130                 135                 140

Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn
145                 150                 155                 160

Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp
                165                 170                 175

Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp
            180                 185                 190

Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp
        195                 200                 205

Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly
    210                 215                 220

Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile
225                 230                 235                 240

Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln
                245                 250                 255

Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val
            260                 265                 270

Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly
        275                 280                 285

Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr
```

```
    290                 295                 300

Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu
305                 310                 315                 320

Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu
                325                 330                 335

Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser
            340                 345                 350

Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys
        355                 360                 365

Gly Val Gln Lys Glu Met Gly Asn
    370                 375


<210>  4
<211>  115
<212>  PRT
<213>  Soybean

<400>  4
Leu Phe Gly Leu Leu Ala Ile Leu Leu Glu Tyr Leu Glu Lys Met Val
1               5                   10                  15

Pro Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro Ser Glu
            20                  25                  30

Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp Val Leu
        35                  40                  45

Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile
    50                  55                  60

Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn
65                  70                  75                  80

Leu Ile Ser Val Leu Val His Cys Asp Ile Arg Gly Ser Glu Val Ile
                85                  90                  95

Leu Gly Asp Asn Ser His Ile His Ile Tyr Glu Asn Gly Gly Ile Ala
            100                 105                 110

Thr Leu Gly
        115


<210>  5
<211>  127
<212>  PRT
<213>  Rice

<220>
<221>  misc_feature
<222>  (4)..(4)
```

<223> Xaa at position 4 can be any naturally occurring amino acid

<400> 5
Lys Thr Leu Xaa Gly Gly Met Arg Gln Val Gly Ile Leu Cys Ala Ala
1 5 10 15

Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Gln Ser Asp His
20 25 30

Asn Lys Ala Lys Leu Leu Ala Asp Gly Leu Asn Glu Ile Lys Gly Leu
35 40 45

Arg Val Asp Ile Ser Ser Val Glu Thr Asn Ile Ile Tyr Val Glu Val
50 55 60

Glu Glu Gly Ser Arg Ala Thr Ala Ala Lys Leu Cys Lys Asp Leu Glu
65 70 75 80

Asp Tyr Gly Ile Leu Leu Met Pro Met Gly Ser Ser Arg Leu Arg Ile
85 90 95

Val Phe His His Gln Ile Ser Ala Ser Asp Val Gln Tyr Ala Leu Ser
100 105 110

Cys Phe Gln Gln Ala Val Asn Gly Val Arg Asn Glu Asn Gly Asn
115 120 125

<210> 6
<211> 147
<212> PRT
<213> Rice

<400> 6
Gly Arg Arg Phe Arg Ala Ile Arg Asp Pro Met Gly Glu Leu Phe Tyr
1 5 10 15

Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn Thr His Ala Asn Ser Gly
20 25 30

Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp Arg Val Gly Glu Leu Ala
35 40 45

Lys Lys His Gly Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn
50 55 60

Ala Ser Val Ala Leu Gly Val Pro Val Asp Arg Leu Val Gln Ala Ala
65 70 75 80

Asp Ser Val Ser Val Cys Leu Ser Lys Gly Ile Gly Ala Pro Val Gly
85 90 95

Ser Val Ile Val Gly Ser Lys Asn Phe Ile Ala Lys Ala Arg Arg Leu
100 105 110

Arg Lys Thr Leu Gly Gly Gly Met Arg Gln Ile Gly Leu Leu Cys Ala

```
        115                 120                 125

Ala Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Glu Ser Asp
    130                 135                 140

His Lys Lys
145
```

<210> 7
<211> 169
<212> PRT
<213> Canola

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa at position 5 can be any naturally occurring amino acid

<400> 7

```
Gly Ile Pro Gly Xaa Thr Phe Arg Gly Asp Val Ala Lys Ser His Gly
1               5                   10                  15

Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn Ala Ser Val Ala
            20                  25                  30

Leu Gly Val Pro Val His Arg Leu Val Lys Ala Ala Asp Ser Val Ser
        35                  40                  45

Val Cys Ile Ser Lys Gly Leu Gly Ala Pro Val Gly Ser Val Ile Val
    50                  55                  60

Gly Ser Thr Ala Phe Ile Glu Lys Ala Lys Ile Leu Thr Lys Thr Leu
65                  70                  75                  80

Gly Gly Gly Met Arg Gln Val Gly Ile Leu Cys Ala Ala Ala Tyr Val
                85                  90                  95

Ala Val Arg Asp Thr Val Gly Lys Leu Ala Asp Asp His Arg Arg Ala
            100                 105                 110

Lys Val Leu Ala Asp Gly Leu Lys Lys Ile Lys His Phe Arg Val Asp
        115                 120                 125

Thr Thr Ser Val Glu Thr Asn Met Val Phe Phe Asp Ile Val Asp Ser
    130                 135                 140

Arg Ile Ser Pro Asp Lys Leu Cys Gln Val Leu Glu Gln Arg Asn Val
145                 150                 155                 160

Leu Ala Met Pro Ala Gly Ser
```